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- (71) Applicant: **PE CORPORATION (NY)** [US/US]; 761
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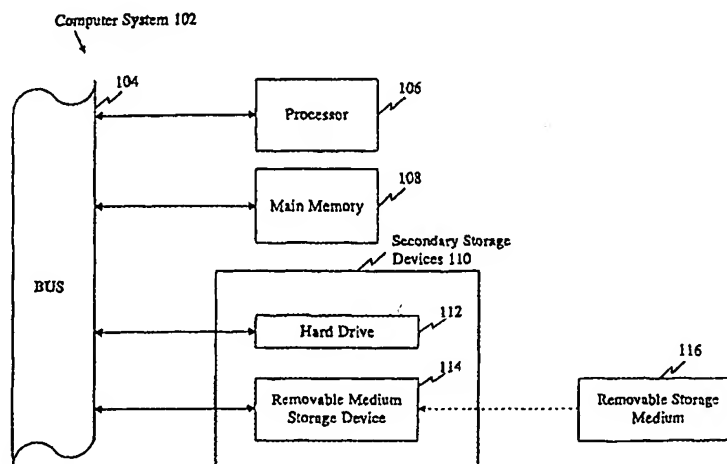
- (72) Inventors: **VENTER, Craig, J.**; Celera Genomics, 45 West Gude Drive C2-4#21, Rockville, MD 20850 (US). **ADAMS, Mark**; Celera Genomics, 45 West Gude Drive C2-4#21, Rockville, MD 20850 (US). **LI, Peter, W., D.**; Celera Genomics, 45 West Gude Drive C2-4#21, Rockville, MD 20850 (US). **MYERS, Eugene, W.**; Celera Genomics, 45 West Gude Drive C2-4#21, Rockville, MD 20850 (US).

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(54) Title: **KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN EXONS OR TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF**



(57) Abstract: The present invention is based on the sequencing and assembly of the human genome. The present invention provides the primary nucleotide sequence of the coding portion of the human genome in the form of a series of transcript sequences with accompanying exon information. This information can be used to generate nucleic acid detection reagents and kits such as nucleic acid arrays, and for other uses.

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CQ728483
 LOCUS CQ728483 884 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 14417 from Patent WO02068579.
 ACCESSION CQ728483
 VERSION CQ728483.1 GI:42297418
 KEYWORDS .
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1
 AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
 TITLE Kits, such as nucleic acid arrays, comprising a majority of
 humanexons or transcripts, for detecting expression and other uses
 thereof
 JOURNAL Patent: WO 02068579-A 14417 06-SEP-2002;
 PE Corporation (NY) (US)

FEATURES Location/Qualifiers
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 /mol_type="unassigned DNA"
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ORIGIN

Query Match 9.4%; Score 298; DB 6; Length 884;
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Db	427	GGGAATTCAGAGACAGCTGATAACAAATATGCATCCATCACCACCAGCTTCAAGGAAT	484

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 Hominidae; Homo.
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 PE Corporation (NY) (US)
 FEATURES Location/Qualifiers
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ORIGIN

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Best Local Similarity:	100.00%	Mismatches:	0
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US-10-792-307-4 (1-906) x CQ728483 (1-884)

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Qy	331	GlyTrpLeuArgTyrArgLeuProMetAlaTyrPheMetValGlyValSerValPheGly	350
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Qy	351	TyrSerLeuIleIleValIleArgSerMetAlaSerAsnThrGlnGlySerThrGlyGlu	370
Db	307	TACAGCCTGATTATTGTTCATTCGATCGATGGCCAGCAATACCCAAGGAAGCACAGGCGAA	366
Qy	371	GlyGluSerAspAsnPheThrPheSerPheLysMetPheThrSerTrpAspTyrLeuIle	390
Db	367	GGGGAGAGTGACAACCTTCACATTCAGCTTCAAGATGTTCAACAGCTGGGACTACCTGATC	426
Qy	391	GlyAsnSerGluThrAlaAspAsnLysTyrAlaSerIleThrThrSerPheLysGlu	409
Db	427	GGGAATTCAGAGACAGCTGATAACAAATATGCATCCATCACCACCAGCTTCAAGGAA	483